



EAGIP5.001APC.TXT

SEQUENCE LISTING

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Lo, Wai Hung

<120> PHARMACEUTICAL PREPARATION AND METHOD OF  
TREATMENT OF HUMAN MALIGNANCIES WITH ARGININE DEPRIVATION

<130> EAGIP5.001APC

<140> 10/518,223

<141> 2004-12-15

<150> PCT/GB2003/002665

<151> 2003-06-20

<150> PCT/CN02/00635

<151> 2002-09-09

<150> 60/390,757

<151> 2002-06-20

<160> 9

<170> FastSEQ for windows Version 4.0

<210> 1

<211> 2002

<212> DNA

<213> Homo sapiens

<400> 1

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acggagaata	tttattggaa	ttaagagtct	ctgggactgc	tcctgtaaat	gctccttgta	180
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agggttaagaa	atttgaaata	gttactattc	tttcccatga	cgtagaaaat	caaaagatta	300
taacagaatg	ggagtcactc	cccagagagg	ctttaccgga	acaatttgat	tcataagaac	360
taattagtag	cgttttccaa	tggaggcgct	ttttattttg	ggtagttgca	taccactaaa	420
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gagggattca	tagatgcata	accatcacca	tcatatgagc	gccaaagtcca	gaaccatagg	660
gattattgga	gctcctttct	caaagggaca	gccacgagga	ggggtggaag	aaggccctac	720
agtattgaga	aaggctgggc	tgcttgagaa	acttaaagaa	caagagtgtg	atgtgaagga	780
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tttgaaaact	ctaggcatta	aatacttttc	atagtactgaa	gtggacagac	taggaattgg	1260
caaggtgatg	gaagaaacac	tcagctatct	actaggaaga	aagaaaaggc	caattcatct	1320
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aactcgaaca	gtgaacacag	cagttgcaat	aaccttggt	tgtttcggac	ttgctcggga	1560
gggtaatcac	aagcctattg	actaccttaa	cccacctaa	taaatgtgga	aacatccgat	1620
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tatattttct aacttgga aagacttatc cttagaaaga gaagtgtaca ttgattttcca 1860
attaaaaaatt tgctggcatt aaaaataagc acacttacat aagcccccat acatagagtg 1920
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attcaaaaaa tgtgattcta ga 2002

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&lt;210&gt; 2

&lt;211&gt; 990

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Chimeric DNA sequence encoding human arginase I  
and an N-terminal histidine tag

&lt;400&gt; 2

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att att gga gct cct ttc tca aag gga cag cca cga gga ggg gtg gaa 96
gaa ggc cct aca gta ttg aga aag gct ggt ctg ctt gag aaa ctt aaa 144
gaa caa gag tgt gat gtg aag gat tat ggg gac ctg ccc ttt gct gac 192
atc cct aat gac agt ccc ttt caa att gtg aag aat cca agg tct gtg 240
gga aaa gca agc gag cag ctg gct ggc aag gtg gca caa gtc aag aag 288
aac gga aga atc agc ctg gtg ctg ggc gga gac cac agt ttg gca att 336
gga agc atc tct ggc cat gcc agg gtc cac cct gat ctt gga gtc atc 384
tgg gtg gat gct cac act gat atc aac act cca ctg aca acc aca agt 432
gga aac ttg cat gga caa cct gta tct ttc ctc ctg aag gaa cta aaa 480
gga aag att ccc gat gtg cca gga ttc tcc tgg gtg act ccc tgt ata 528
tct gcc aag gat att gtg tat att ggc ttg aga gac gtg gac cct ggg 576
gaa cac tac att ttg aaa act cta ggc att aaa tac ttt tca atg act 624
gaa gtg gac aga cta gga att ggc aag gtg atg gaa gaa aca ctc agc 672
tat cta cta gga aga aag aaa agg cca att cat cta agt ttt gat gtt 720
gac gga ctg gac cca tct ttc aca cca gct act ggc aca cca gtc gtg 768
gga ggt ctg aca tac aga gaa ggt ctc tac atc aca gaa gaa atc tac 816
aaa aca ggg cta ctc tca gga tta gat ata atg gaa gtg aac cca tcc 864
ctg ggg aag aca cca gaa gaa gta act cga aca gtg aac aca gca gtt 912
gca ata acc ttg gct tgt ttc gga ctt gct cgg gag ggt aat cac aag 960
cct att gac tac ctt aac cca cct aag taa 990

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&lt;210&gt; 3

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Chimeric AA sequence of human arginase I and an  
N-terminal histidine tag

&lt;400&gt; 3

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Ile Ile Gly Ala Pro Phe Ser Lys Gly Gln Pro Arg Gly Gly Val Glu
20      25      30
Glu Gly Pro Thr Val Leu Arg Lys Ala Gly Leu Leu Glu Lys Leu Lys
35      40      45
Glu Gln Glu Cys Asp Val Lys Asp Tyr Gly Asp Leu Pro Phe Ala Asp
50      55      60
Ile Pro Asn Asp Ser Pro Phe Gln Ile Val Lys Asn Pro Arg Ser Val
65      70      75      80
Gly Lys Ala Ser Glu Gln Leu Ala Gly Lys Val Ala Gln Val Lys Lys
85      90      95
Asn Gly Arg Ile Ser Leu Val Leu Gly Asp His Ser Leu Ala Ile
100     105     110

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EAGIP5.001APC.TXT

Gly Ser Ile Ser Gly His Ala Arg Val His Pro Asp Leu Gly Val Ile  
 115 120 125  
 Trp Val Asp Ala His Thr Asp Ile Asn Thr Pro Leu Thr Thr Thr Ser  
 130 135 140  
 Gly Asn Leu His Gly Gln Pro Val Ser Phe Leu Leu Lys Glu Leu Lys  
 145 150 155 160  
 Gly Lys Ile Pro Asp Val Pro Gly Phe Ser Trp Val Thr Pro Cys Ile  
 165 170 175  
 Ser Ala Lys Asp Ile Val Tyr Ile Gly Leu Arg Asp Val Asp Pro Gly  
 180 185 190  
 Glu His Tyr Ile Leu Lys Thr Leu Gly Ile Lys Tyr Phe Ser Met Thr  
 195 200 205  
 Glu Val Asp Arg Leu Gly Ile Gly Lys Val Met Glu Glu Thr Leu Ser  
 210 215 220  
 Tyr Leu Leu Gly Arg Lys Lys Arg Pro Ile His Leu Ser Phe Asp Val  
 225 230 235 240  
 Asp Gly Leu Asp Pro Ser Phe Thr Pro Ala Thr Gly Thr Pro Val Val  
 245 250 255  
 Gly Gly Leu Thr Tyr Arg Glu Gly Leu Tyr Ile Thr Glu Glu Ile Tyr  
 260 265 270  
 Lys Thr Gly Leu Leu Ser Gly Leu Asp Ile Met Glu Val Asn Pro Ser  
 275 280 285  
 Leu Gly Lys Thr Pro Glu Glu Val Thr Arg Thr Val Asn Thr Ala Val  
 290 295 300  
 Ala Ile Thr Leu Ala Cys Phe Gly Leu Ala Arg Glu Gly Asn His Lys  
 305 310 315 320  
 Pro Ile Asp Tyr Leu Asn Pro Pro Lys  
 325

<210> 4  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> 6x Histidine tag

<400> 4  
 Met His His His His His His  
 1 5

<210> 5  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide primer sequence

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33

<210> 6  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide primer sequence

<400> 6

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<210> 7

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide primer sequence

<400> 7

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<210> 8

<211> 969

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(969)

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aag gga cag cca cga gga ggg gtg gaa gaa ggc cct aca gta ttg aga 96  
Lys Gly Gln Pro Arg Gly Gly Val Glu Glu Gly Pro Thr Val Leu Arg  
20 25 30

aag gct ggt ctg ctt gag aaa ctt aaa gaa caa gag tgt gat gtg aag 144  
Lys Ala Gly Leu Leu Glu Lys Leu Lys Glu Gln Glu Cys Asp Val Lys  
35 40 45

gat tat ggg gac ctg ccc ttt gct gac atc cct aat gac agt ccc ttt 192  
Asp Tyr Gly Asp Leu Pro Phe Ala Asp Ile Pro Asn Asp Ser Pro Phe  
50 55 60

caa att gtg aag aat cca agg tct gtg gga aaa gca agc gag cag ctg 240  
Gln Ile Val Lys Asn Pro Arg Ser Val Gly Lys Ala Ser Glu Gln Leu  
65 70 75 80

gct ggc aag gtg gca caa gtc aag aag aac gga aga atc agc ctg gtg 288  
Ala Gly Lys Val Ala Gln Val Lys Lys Asn Gly Arg Ile Ser Leu Val  
85 90 95

ctg ggc gga gac cac agt ttg gca att gga agc atc tct ggc cat gcc 336  
Leu Gly Gly Asp His Ser Leu Ala Ile Gly Ser Ile Ser Gly His Ala  
100 105 110

agg gtc cac cct gat ctt gga gtc atc tgg gtg gat gct cac act gat 384  
Arg Val His Pro Asp Leu Gly Val Ile Trp Val Asp Ala His Thr Asp  
115 120 125

atc aac act cca ctg aca acc aca agt gga aac ttg cat gga caa cct 432  
Ile Asn Thr Pro Leu Thr Thr Thr Ser Gly Asn Leu His Gly Gln Pro  
130 135 140

gta tct ttc ctc ctg aag gaa cta aaa gga aag att ccc gat gtg cca 480  
Val Ser Phe Leu Leu Lys Glu Leu Lys Gly Lys Ile Pro Asp Val Pro  
145 150 155 160

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att ggc ttg aga gac gtg gac cct ggg gaa cac tac att ttg aaa act	576
Ile Gly Leu Arg Asp Val Asp Pro Gly Glu His Tyr Ile Leu Lys Thr	
	180 185 190
cta ggc att aaa tac ttt tca atg act gaa gtg gac aga cta gga att	624
Leu Gly Ile Lys Tyr Phe Ser Met Thr Glu Val Asp Arg Leu Gly Ile	
	195 200 205
ggc aag gtg atg gaa gaa aca ctc agc tat cta cta gga aga aag aaa	672
Gly Lys Val Met Glu Glu Thr Leu Ser Tyr Leu Leu Gly Arg Lys Lys	
	210 215 220
agg cca att cat cta agt ttt gat gtt gac gga ctg gac cca tct ttc	720
Arg Pro Ile His Leu Ser Phe Asp Val Asp Gly Leu Asp Pro Ser Phe	
	225 230 235 240
aca cca gct act ggc aca cca gtc gtg gga ggt ctg aca tac aga gaa	768
Thr Pro Ala Thr Gly Thr Pro Val Val Gly Gly Leu Thr Tyr Arg Glu	
	245 250 255
ggt ctc tac atc aca gaa gaa atc tac aaa aca ggg cta ctc tca gga	816
Gly Leu Tyr Ile Thr Glu Glu Ile Tyr Lys Thr Gly Leu Leu Ser Gly	
	260 265 270
tta gat ata atg gaa gtg aac cca tcc ctg ggg aag aca cca gaa gaa	864
Leu Asp Ile Met Glu Val Asn Pro Ser Leu Gly Lys Thr Pro Glu Glu	
	275 280 285
gta act cga aca gtg aac aca gca gtt gca ata acc ttg gct tgt ttc	912
Val Thr Arg Thr Val Asn Thr Ala Val Ala Ile Thr Leu Ala Cys Phe	
	290 295 300
gga ctt gct cgg gag ggt aat cac aag cct att gac tac ctt aac cca	960
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cct aag taa	969
Pro Lys *	

<210> 9  
 <211> 322  
 <212> PRT  
 <213> Homo sapiens

<400> 9  
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 35 40 45  
 Asp Tyr Gly Asp Leu Pro Phe Ala Asp Ile Pro Asn Asp Ser Pro Phe  
 50 55 60  
 Gln Ile Val Lys Asn Pro Arg Ser Val Gly Lys Ala Ser Glu Gln Leu  
 65 70 75 80  
 Ala Gly Lys Val Ala Gln Val Lys Lys Asn Gly Arg Ile Ser Leu Val  
 85 90 95

## EAGIP5.001APC.TXT

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		115					120					125			
Ile	Asn	Thr	Pro	Leu	Thr	Thr	Thr	Ser	Gly	Asn	Leu	His	Gly	Gln	Pro
	130					135					140				
Val	Ser	Phe	Leu	Leu	Lys	Glu	Leu	Lys	Gly	Lys	Ile	Pro	Asp	Val	Pro
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Gly	Phe	Ser	Trp	Val	Thr	Pro	Cys	Ile	Ser	Ala	Lys	Asp	Ile	Val	Tyr
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Ile	Gly	Leu	Arg	Asp	Val	Asp	Pro	Gly	Glu	His	Tyr	Ile	Leu	Lys	Thr
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Leu	Gly	Ile	Lys	Tyr	Phe	Ser	Met	Thr	Glu	Val	Asp	Arg	Leu	Gly	Ile
		195					200					205			
Gly	Lys	Val	Met	Glu	Glu	Thr	Leu	Ser	Tyr	Leu	Leu	Gly	Arg	Lys	Lys
	210					215					220				
Arg	Pro	Ile	His	Leu	Ser	Phe	Asp	Val	Asp	Gly	Leu	Asp	Pro	Ser	Phe
225					230					235					240
Thr	Pro	Ala	Thr	Gly	Thr	Pro	Val	Val	Gly	Gly	Leu	Thr	Tyr	Arg	Glu
				245					250					255	
Gly	Leu	Tyr	Ile	Thr	Glu	Glu	Ile	Tyr	Lys	Thr	Gly	Leu	Leu	Ser	Gly
			260					265					270		
Leu	Asp	Ile	Met	Glu	Val	Asn	Pro	Ser	Leu	Gly	Lys	Thr	Pro	Glu	Glu
		275					280					285			
Val	Thr	Arg	Thr	Val	Asn	Thr	Ala	Val	Ala	Ile	Thr	Leu	Ala	Cys	Phe
	290					295					300				
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305					310					315					320
Pro	Lys														